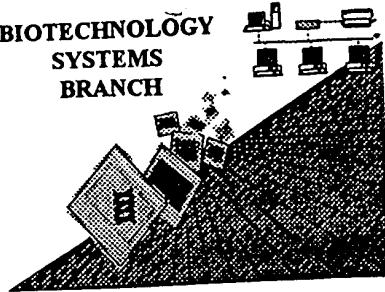


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/591,449

BEST AVAILABLE COPY

Source:

01PK

Date Processed by STIC:

6/16/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY
EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT
COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY
or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT,
WITH A NOTICE TO COMPLY

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,
703-308-4212.**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:**

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/591447</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics	<p>The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".</p>	
2 <input type="checkbox"/> Wrapped Aminos	<p>The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".</p>	
3 <input type="checkbox"/> Incorrect Line Length	<p>The rules require that a line not exceed 72 characters in length. This includes spaces.</p>	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	<p>The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.</p>	
5 <input checked="" type="checkbox"/> Non-ASCII	<p>This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.</p>	
6 <input type="checkbox"/> Variable Length	<p>Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.</p>	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	<p>A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/>. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.</p>	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	<p>Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped</p> <p>Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).</p>	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	<p>Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000</p>	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	<p>Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.</p>	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	<p>Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response.</p>	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	<p>Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)</p>	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	<p>Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.</p>	

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/591,447

DATE: 06/16/2000
TIME: 18:49:59

Input Set : A:\PTO-SG.txt
Output Set: N:\CRF3\06162000\I591447.raw

*See line 5 on Enclosed
Summary Sheet*

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING
4 (1) GENERAL INFORMATION:
E--> 6 (i) APPLICANT:
14 (ii) TITLE OF INVENTION: VACCINES CONTAINING ATTENUATED BACTERIA
16 (iii) NUMBER OF SEQUENCES: 4
E--> 0 (iv) CORRESPONDENCE ADDRESS:
8 (B) STREET: 10 St James's Street
9 (C) CITY: London
10 (D) STATE: not applicable
11 (E) COUNTRY: United Kingdom
C--> 12 (F) ZIP: SW1A 1EP
C--> 18 (v) COMPUTER READABLE FORM:
19 (A) MEDIUM TYPE: Floppy disk
20 (B) COMPUTER: IBM PC compatible
21 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
C--> 0 (vi) CURRENT APPLICATION DATA:
C--> 0 (A) APPLICATION NUMBER: US/09/591,447
C--> 0 (B) FILING DATE: 09-Jun-2000
C--> 0 (viii) ATTORNEY/AGENT INFORMATION:
7 (A) NAME: Medeva Europe Limited

*Submitted file was in
bold print - eliminate
bold print
All following pages*

ERRORED SEQUENCES

371 (2) INFORMATION FOR SEQ ID NO: 4:
373 (i) SEQUENCE CHARACTERISTICS:
374 (A) LENGTH: 428 amino acids
375 (B) TYPE: amino acid
376 (D) TOPOLOGY: linear
378 (ii) MOLECULE TYPE: protein
379 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
381 Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn
382 1 5 10 15
384 Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val
385 20 25 30
386 Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser
387 35 40 45
389 Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala
390 50 55 60
392 Thr Leu Arg His Gln Ile Met Glu Arg Leu Ile Met Asp Gln Ile Ile
393 65 70 75 80
395 Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Ser Asp Glu Gln Leu
396 85 90 95
398 Asp Gln Ala Ile Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Leu Asp
399 100 105 110
401 Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Asn Thr Tyr

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/591,447

DATE: 06/16/2000
TIME: 18:49:59

Input Set : A:\PTO-SG.txt
Output Set: N:\CRF3\06162000\I591447.raw

```

402      115          120          125
404 Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn
405      130          135          140
407 Glu Val Arg Arg Arg Ile Thr Ile Leu Pro Gln Glu Val Glu Ser Leu
408 145      150          155          160
410 Ala Gln Gln Val Gly Asn Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu
411      165          170          175
413 Ser His Ile Leu Ile Pro Leu Pro Glu Asn Pro Thr Ser Asp Gln Val
414      180          185          190
416 Asn Glu Ala Glu Ser Gln Ala Arg Ala Ile Val Asp Gln Ala Arg Asn
417      195          200          205
419 Gly Ala Asp Phe Gly Lys Leu Ala Ile Ala His Ser Ala Asp Gln Gln
420      210          215          220
422 Ala Leu Asn Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro
423 225      230          235          240
425 Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val
426      245          250          255
428 Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp
429      260          265          270
431 Leu Arg Gly Glu Ser Lys Asn Ile Ser Val Thr Glu Val His Ala Arg
432      275          280          285
434 His Ile Leu Leu Lys Pro Ser Pro Ile Met Thr Asp Glu Gln Ala Arg
435      290          295          300
437 Val Lys Leu Glu Gln Ile Ala Ala Asp Ile Glu Ser Gly Lys Thr Thr
438 305      310          315          320
440 Phe Ala Ala Ala Thr Lys Glu Phe Ser Gln Asp Pro Val Ser Ala Asn
441      325          330          335
443 Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala
444      340          345          350
446 Phe Arg Asp Ala Leu Thr Arg Leu Asn Lys Gly Gln Met Ser Ala Pro
447      355          360          365
449 Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg
450      370          375          380
452 Asn Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met
453 385      390          395          400
455 Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Ser Trp Met Gln Glu
456      405          410          415
458 Gln Arg Ala Ser Ala Tyr Val Lys Ile Leu Ser Asn
459      420          425
E--> 464 7

```

delete at end of file

see following page for more errors

Sequence listing

SEQUENCE LISTING

09/591,447

(1) GENERAL INFORMATION:

(i) APPLICANT: *Priority - all responses must be on same line as heading*

(A) NAME: Medeva Europe Limited
(B) STREET: 10 St James's Street
(C) CITY: London
(D) STATE: not applicable
(E) COUNTRY: United Kingdom
(F) POSTAL CODE (ZIP): SW1A 1EE

(ii) TITLE OF INVENTION: VACCINES CONTAINING ATTENUATED BACTERIA

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

(J) (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

*Add these MANDATORY
headings and
responses for a U.S.
Case*

(v) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

Add these mandatory headings for a U.S. case

*Fig 1: EPO format of PatentIn is invalid
for a U.S. case*

VERIFICATION SUMMARY DATE: 06/16/2000
PATENT APPLICATION: US/09/591,447 TIME: 18:50:00

Input Set : A:\PTO-SG.txt
Output Set: N:\CRF3\06162000\I591447.raw

L:12 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
L:18 M:220 C: Keyword misspelled or invalid format, [(v) COMPUTER READABLE FORM:]
L:6 M:200 E: Mandatory Header Field missing, [(i) APPLICANT:] Value not provided
L:0 M:200 E: Mandatory Header Field missing, [(A) ADDRESSEE:]
L:0 M:248 E: Inserted missing Mandatory Header Field, [(iv) CORRESPONDENCE ADDRESS:]
L:0 M:247 C: Inserted Optional Header Field, [(viii) ATTORNEY/AGENT INFORMATION:]
L:0 M:249 C: Inserted Mandatory Field, [(vi) CURRENT APPLICATION DATA:]
L:0 M:249 C: Inserted Mandatory Field, [(A) APPLICATION NUMBER:]
L:0 M:249 C: Inserted Mandatory Field, [(B) FILING DATE:]
L:264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:284 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:292 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:296 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:300 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:304 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:308 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:312 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:316 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:320 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:324 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:328 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:332 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:336 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:340 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:344 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:348 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:352 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:356 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:360 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:368 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:464 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4